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Neofomitella polyzonata gen. et sp. nov., and *N. fumosipora* and *N. rhodophaea* transferred from *Fomitella*

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Abstract — Phylogenetic analysis based on ITS, nLSU, and RPB2 sequences revealed that *Fomitella* in the current sense belonged to two distantly related subclades in the core polyporoid clade. *Fomitella* in a narrow sense is proposed for the type species, *F. supina*, and *Neofomitella* gen. nov. is proposed for *Fomitella fumosipora* and *F. rhodophaea* and a new species *N. polyzonata*. *Neofomitella* differs from *Fomitella* by its distinctly crusted basidiocarps with the cuticle developing from base to margin. Illustrated descriptions of the new genus and species are provided. The main morphological differences between *Fomitella*, *Neofomitella,* and related genera are discussed, and an identification key to *Neofomitella* is also provided.

Key words — phylogeny, *Polyporaceae*, *Polyporales*, *Basidiomycota*, taxonomy

Introduction

Fomitella Murrill, typified by *F. supina* (Sw.) Murrill, was erected as a monotypic genus by Murrill (1905). Subsequently, *F. fumosoavellanea* (Romell) Murrill [*Trichaptum fumosoavellaneum* (Romell) Rajchenb. & Bianchin.], *F. fumosipora*, *F. rhodophaea*, and *F. malaysiana* (Corner) T. Hatt. & Sotome were transferred to the genus (Murrill 1908; Hattori 2005; Hattori & Sotome 2013). Hattori (2005) emended the generic concept of *Fomitella* as follows: basidiocarps annual to perennial, effused-reflexed to distinctly pileate, pileal surface glabrous to minutely tomentose, context firm-fibrous to corky, light orange to pale brown, with a dark agglutinated crust; hyphal system trimitic with clamped generative hyphae, skeletal and binding hyphae well differentiated, negative in Melzer's reagent; cystidia absent; basidiospores

ellipsoid to cylindrical, colorless, thin-walled, smooth, and negative in Melzer's reagent; causing a white rot.

On-going studies on the diversity of wood-rotting fungi in eastern China have produced several new species (Dai & Cui 2005; Cui & Dai 2008a,b; Cui et al. 2007, 2008; He & Dai 2012; Wang et al. 2009, 2011; Cao et al. 2012), and additional study on the specimens from this area recently revealed an undescribed species. Phylogenetic analysis clustered our undescribed species with *Fomitella fumosipora* and *F. rhodophaea* as a clade separated from *F. supina*. Therefore, we propose a new genus *Neofomitella* to accommodate the new species and two new combinations from *Fomitella*.

Materials & methods

Morphological studies

The studied specimens were deposited at the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC) and Institute of Applied Ecology, Chinese Academy of Sciences (IFP). The microscopic procedure follows Cui & Zhao (2012). To present the basidiospore size variation, 5% of measurements were excluded from each end of the range and were given in parentheses. In the text the following abbreviations were used: IKI = Melzer's reagent, IKI– = both inamyloid and non-dextrinoid, KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n = number of spores measured from given number of specimens. Special colors follow Petersen (1996).

Molecular study and phylogenetic analysis

Dried specimens were used for molecular study. CTAB rapid Plant genome extraction kit-DN14 (Aidlab Biotechnologies Co. Ltd, Beijing) was used to extract DNA, according to the manufacturer's instructions with some modifications. ITS region was amplified with primer pair ITS5 and ITS4 (White et al. 1990), nLSU region with primer pair LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm), and RPB2 with primer pair fRPB2-f5F and bRPB2-7.1R (Liu et al. 1999; Matheny 2005). The PCR procedures were: (1) for ITS — initial denaturation at 95°C for 3 min, followed by 35 cycles at 94°C for 40 s, 54°C for 45 s and 72°C for 1 min, and a final extension of 72°C for 10 min; (2) for nLSU — initial denaturation at 94°C for 1 min, followed by 35 cycles at 94°C for 30 s, 50°C for 1 min and 72°C for 1.5 min, and a final extension of 72°C for 10 min; and (3) for RPB2 — initial denaturation at 94°C for 2 min, followed by 10 cycles at 94°C for 40 s, 60°C for 40 s and 72°C for 2 min, then followed by 37 cycles at 94°C for 45 s, 55°C for 1.5 min and 72°C for 2 min, and a final extension of 72°C for 10 min. The PCR products were directly sequenced in Beijing Genomics Institute, China, with the same primers.

Other reference sequences for our phylogenetic analysis were selected from Binder et al. (2005), Justo & Hibbett (2011), Miettinen & Rajchenberg (2012), and BLAST searches in GenBank (Table 1). These sequences were sampled from *Polyporales* with

Table 1. Polyporalean and outgroup taxa used in phylogenetic analysis.
(Sequences generated in this study are in bold.)

Species	Sample number	ITS	nLSU	RPB2
Abundisporus pubertatis	Dai 11927	**KC867398**	**KC867494**	**KF274654**
Abundisporus violaceus	MUCL38617	FJ411100	FJ393867	—
Climacodon septentrionalis	AFTOL-ID 767	AY854082	AY684165	AY780941
Coriolopsis aspera	Cui 6702	**KC867353**	**KC867476**	**KF274658**
	Cui 6725	**KC867356**	**KC867477**	**KF274659**
Coriolopsis brunneoleuca	Dai 12087	**KC867416**	**KC867435**	**KF274656**
	Dai 12180	**KC867414**	**KC867432**	**KF274655**
Coriolopsis byrsina	FP-105050-Sp	JN165001	JN164788	JN164871
Coriolopsis cf. *caperata*	CR22	JN164999	JN164789	JN164870
	Ryvarden 45481	**KC867399**	**KC867428**	**KF274657**
Coriolopsis retropicta	Dai 9870	**KC867404**	**KC867443**	**KF274653**
Coriolopsis rigida	BJFC12680	**KC867381**	**KC867454**	**KF274664**
Coriolopsis sanguinaria	Cui 5444	**KC867387**	**KC867463**	—
	Dai 9314	**KC867390**	**KC867467**	—
Coriolopsis sp.	BRFM1125	JX082370	—	—
	BRFM1126	JX082371	—	—
Coriolopsis strumosa	Dai 10642	**JX559278**	**JX559303**	**JX559312**
	Dai 10657	**KC867371**	**KC867491**	**KF274650**
Daedaleopsis confragosa	Cui 9732	**JX569731**	**JX569748**	**KF274647**
Daedaleopsis sinensis	Dai 11431	**JX569732**	**JX569749**	**KF274648**
Datronia mollis	RLG6304sp	JN165002	JN164791	JN164872
Datronia scutellata	RLG9584T	JN165004	JN164792	JN164873
Dentocorticium sulphurellum	T609	JN165015	JN164815	JN164875
Donkioporia expansa	P188	HM536087	HM536052	HM536102
Earliella scabrosa	PR1209	JN165009	JN164793	JN164866
Fomes fomentarius	Cui 8020	JX290073	JX290070	—
Fomitella supina	JV0610	**KF274645**	**KF274646**	—
	Nunez 1183	**KF274644**	**—**	—
	Ryvarden 39027	**KF274643**	—	—
Fomitopsis pinicola	AFTOL-ID 770	AY854083	AY684164	AY786056
Funalia gallica	BJFC12697	**KC867379**	**KC867453**	—
	RLG-7630-sp	JN165013	JN164814	JN164869
Funalia trogii	RLG-4286-Sp	JN164993	JN164808	JN164867
Ganoderma tsugae	AFTOL-ID 771	DQ206985	AY684163	DQ408116
Grifola sordulenta	AFTOL-ID 562	AY854085	AY645050	AY786058
Hexagonia apiaria	Cui 6447	KC867362	KC867481	KF274660
Hexagonia glabra	Cui 8468	**JX559277**	**JX559302**	**JX559311**
	Dai 10991	**JX569733**	**JX569750**	**KF274649**
Lignosus rhinocerotis	PEN94	JQ409359	AB368074	AB368132
Lopharia cinerascens	FP-105043-sp	JN165019	JN164813	JN164874
Megasporia major	Cui 10253	JQ314366	JQ780437	JX559314
Megasporoporiella subcavernulosa	Cui 9252	JQ780378	JQ78041	JX559315
Microporus affinis	Cui 7714	**JX569739**	**JX569746**	**KF274661**
Microporus flabelliformis	Dai 11574	**JX569740**	**JX569747**	**KF274662**
Microporus xanthopus	Cui 8284	JX290074	JX290071	JX559313
Neofomitella fumosipora	Cui 8816	**JX569734**	**JX569741**	—
	Dai 10777	**JX569735**	**JX569742**	—
Neofomitella polyzonata	Dai 10419	**JX569738**	**JX569745**	**KF274663**
	Dai 10420	**JX569736**	**JX569743**	—
	Dai 11360	**JX569737**	**JX569744**	—
Neofomitella rhodophaea	TFRI 414	EU232216	EU232300	—
Perenniporia corticola	Cui 1465	JN048759	JN048779	**KF274651**
Perenniporia tenuis	Wei 2783	JQ001858	JQ001848	**KF274652**
Phlebia radiata	FPL6140	AY854087	AF287885	AY218502
Polyporus grammocephalus	WD2343	AB587626	AB368089	AB368146
Polyporus varius	WD2347	AB587636	AB368111	AB368168
Pseudofavolus cucullatus	WD2157	AB587637	AB368114	AB368170
Trametes betulina	HHB-9942-sp	JN164983	JN164794	JN164860
Trametes elegans	FP-105679-sp	JN164944	JN164799	JN164861
Trametes polyzona	BKW-004	JN164978	JN164790	JN164856
Trametes sanguinea	PR-SC-95	JN164982	JN164795	JN164858
Trametes suaveolens	FP-102529-sp	JN164966	JN164807	JN164853
Trametes versicolor	FP-135156-sp	JN164919	JN164809	JN164850
Trametopsis cervina	TJV-93-216-sp	JN165020	JN164796	JN164877
Boletopsis leucomelaena	AFTOL-ID 1527	DQ484064	DQ154112	GU187820
Hydnellum geogenium	AFTOL-ID 680	DQ218304	AY631900	DQ408133

the aim of providing representatives for all major clades within the order, concluded by Larsson et al. (2004), Binder et al. (2005) and Larsson (2007). *Boletopsis leucomelaena* (Pers.) Fayod and *Hydnellum geogenium* (Fr.) Banker were selected as outgroup (Justo & Hibbett 2011). Phylogenetic analysis for each single gene was carried out, and we got similar topologies to combined dataset in both MP and Bayes analyses. So in the paper we showed the result from the combined dataset that received higher support values. This combined dataset was aligned using Clustalx 1.83 (Chenna et al. 2003) and manually edited as necessary. Sequence alignment was deposited at TreeBase (submission ID 14418).

Maximum parsimony (MP) analysis was performed using PAUP* 4.0b10 (Swofford 2002) with gaps treated as missing data. Trees were generated using 100 replicates of random stepwise addition of sequence and tree-bisection reconnection (TBR) branch-swapping algorithm. All characters were given equal weight. Branch support for all parsimony analysis was estimated by performing 1 000 bootstrap (BP) replicates (Felsenstein 1985) with a heuristic search of 10 random-addition replicates for each bootstrap replicate.

The best-fit model of nucleotide substitution was selected by hierarchical likelihood ratio tests (hLRT, Huelsenbeck & Crandall 1997; Posada & Crandall 2001) implemented in the MrModelTest 2.2 (Posada & Crandall 1998; Nylander 2004). Following this model, MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003) was used for Bayesian inference (BI). Eight Markov chains were run from random starting tree for 3,000,000 generations and sampled every 100 generations. The first one-fourth of the trees, which represented the burn-in phase of the analysis, were discarded, while the last three-fourths were used for calculating Bayesian posterior probabilities (BPPs) in the consensus tree. Confident branch support is defined as BPPs not less than 0.95 and bootstrap values above 50%.

Results

Molecular phylogeny

The combined dataset included 66 samples with 66 ITS, 62 nLSU, and 51 RPB2 sequences, representing 50 species and two collections not identified to species level from the main clades of *Polyporales*, as well as two species from *Thelephorales* as outgroup. MP analysis yielded eight equally parsimonious trees (tree length = 9 153, CI = 0.283, RI = 0.520, RC = 0.147, HI = 0.717). The best model for the alignment was estimated as "GTR+I+G". BI resulted in an average standard deviation of split frequencies 0.005127. The topologies from MP and BI were similar, and only the BI tree was presented along with the BP from MP analysis (Fig. 1). In the phylogenetic analysis, sampled species of *Fomitella* formed two subclades within the core polyporoid clade. One subclade comprised *Fomitella supina*, the generic type, and two unidentified collections (labelled as *Coriolopsis*) from French Guiana (BPP = 1.00, MP = 100%; Fig. 1), while the second subclade included *F. fumosipora*, *F. rhodophaea* and our undescribed species (BPP = 1.00, MP = 96%; Fig. 1). Taken the morphology into consideration together, we propose a new genus, *Neofomitella*, to accommodate

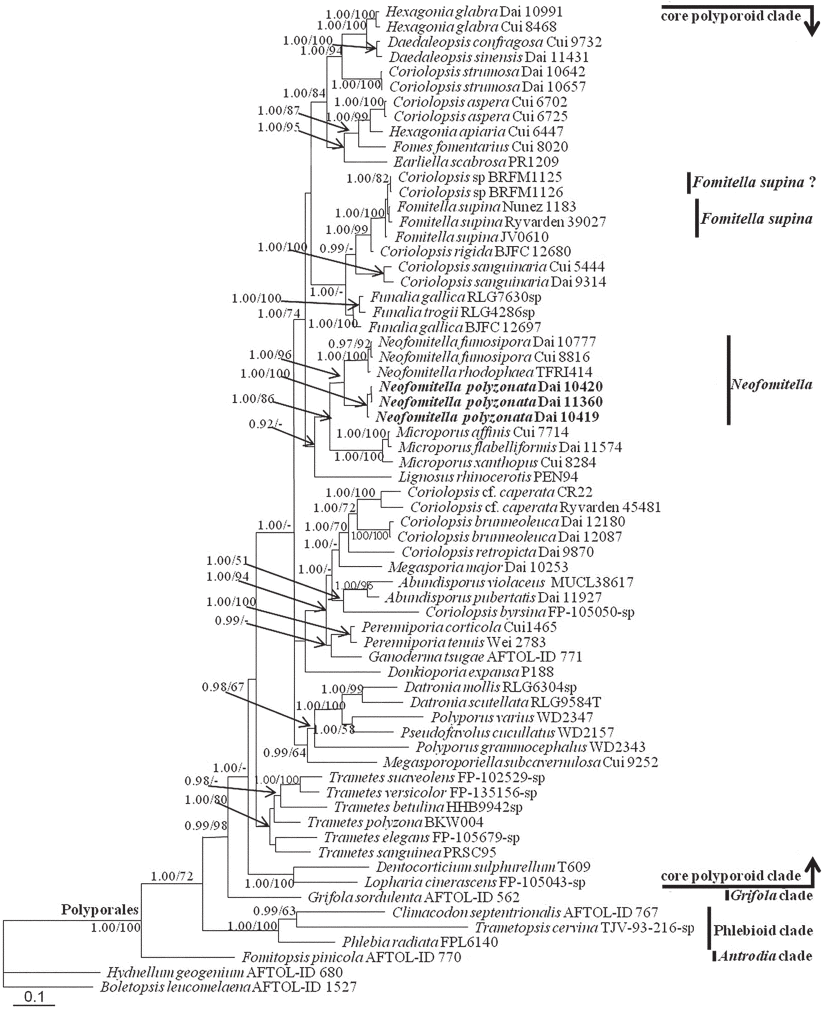

Fig. 1. Phylogram of polyporalean taxa obtained from Bayesian inference of the combined dataset of ITS, nLSU, and RPB2. Bayesian posterior probabilities more than 0.95 and bootstrap values above 50% are indicated above or below the branches. The scale bar represents estimated number of changes per site.

the second subclade; we transfer the two *Fomitella* species to the new genus and describe our new species as *N. polyzonata*. Phylogenetically, the *Neofomitella* subclade clusters with a *Microporus* subclade (Fig. 1).

Taxonomy

Neofomitella Y.C. Dai, Hai J. Li & Vlasák, **gen. nov.**

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Differs from *Fomitella* by its distinctly crusted basidiocarps with the cuticle developing from base to margin and from *Microporus* by its buff, yellowish brown, brown to pale grey context.

Type species — *Polyporus rhodophaeus* Lév.

Etymology — *Neofomitella* (Lat.): referring to the morphological similarity to *Fomitella*.

Basidiocarps annual or perennial, pileate, sessile or effused-reflexed. Pileal surface yellowish-brown, brown, orange-brown, reddish-brown, fuscous to almost black, usually concentrically zonate or sulcate, glabrous to velutinate. Context buff, yellowish brown, brown to pale grey, corky to hard corky, with a dark agglutinated crust developing from base to margin. Pore surface usually white, cream to pale buff when fresh, pale brown to yellowish-brown when dry. Hyphal system trimitic with clamped generative hyphae, skeletal and binding hyphae well differentiated, negative in Melzer's reagent. Cystidia absent. Basidiospores oblong ellipsoid to cylindrical, hyaline, thin-walled, smooth, IKI–, CB–, tissue turn into black in KOH. Growing usually on angiosperm wood and causing a white rot.

Neofomitella fumosipora (Corner) Y.C. Dai, Hai J. Li & Vlasák, **comb. nov.** Fig. 2a

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≡*Trametes fumosipora* Corner, Beih. Nova Hedwigia 97: 106 (1989).

≡*Fomitella fumosipora* (Corner) T. Hatt., Mycoscience 46: 309 (2005).

Specimens examined — **CHINA**. **Guangdong Province**, Shixing County, Chebaling Nature Reserve, fallen angiosperm trunk, 25 Jun 2010, B.K. Cui 8816 (BJFC 7756); 23 Nov 2010, B.K. Cui 8715, 8717 (BJFC 7657, 7659); **Hainan Province**, Changjiang County, Bawangling Nature Reserve, fallen angiosperm trunk, 8 May 2009, Y.C. Dai 10777 (BJFC 5021). **MALAYSIA**. **Negeri Sembilam**, Pasoh For. Res., 5 Dec 1998, T. Hattori (BJFC: ex. TFM ex. F. 19017); **Penang**, Penang Hill, alt. 500–750 m, 13 Dec 2002, T. Hattori (BJFC: ex. TFM ex. F. 20477).

Neofomitella polyzonata Y.C. Dai, Hai J. Li & Vlasák, **sp. nov.** Figs 2b,c, 3

MycoBank MB 804804

Differs from *Neofomitella fumosipora* and *N. rhodophaea* by its distinctly velutinate pileal surface and larger pores.

Type — China, Jiangxi Province, Fenyi County, Dagang Mountain, on fallen trunk of *Cyclobalanopsis blakei* (Skan) Schottky (*Fagaceae*), 18 Sep 2008, Y.C. Dai 10419 (**holotype**, BJFC 4668).

Etymology — *polyzonata* (Lat.): referring to the multiple zones on the pileal surface.

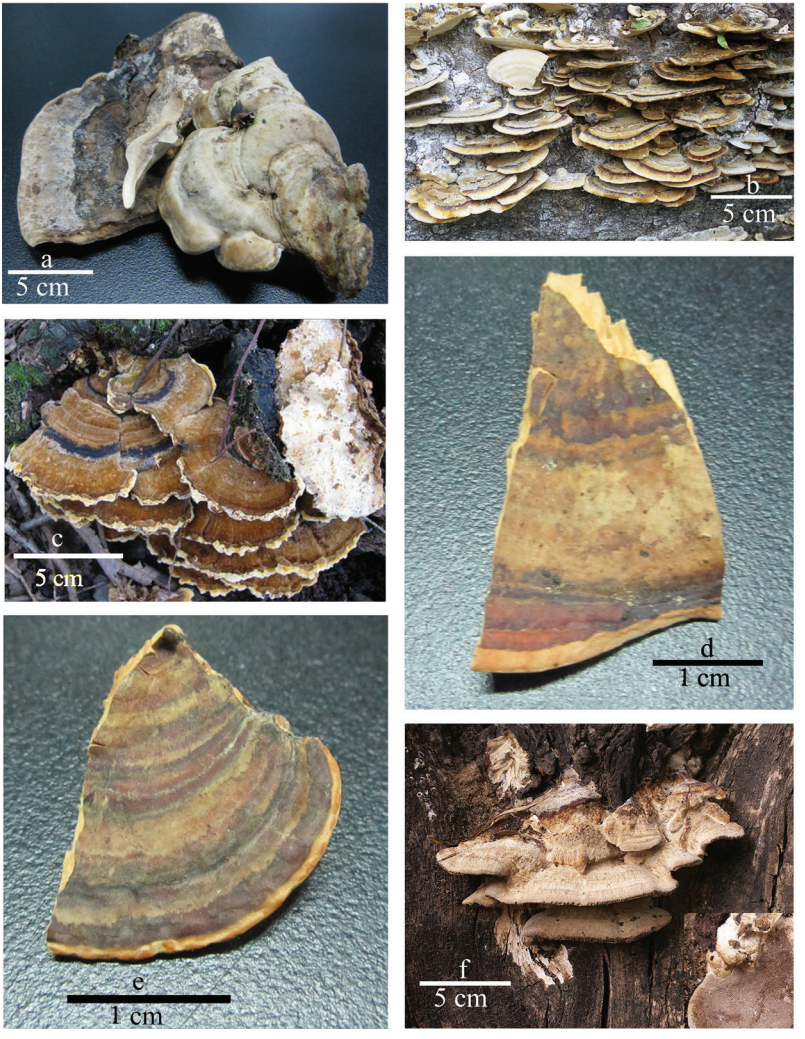

Fig. 2. *Neofomitella* and *Fomitella* basidiocarps. a: *N. fumosipora*. b, c: *N. polyzonata*. d, e: *N. rhodophaea*. f: *F. supina*.

Fruitbody — Basidiocarps annual, pileate, sessile, usually imbricate, without odor or taste when fresh, hard corky to woody hard and light in weight upon drying. Pilei applanate, semicircular to dimidiate, up to 6 cm long, 10 cm wide and 6 mm thick at base. Pileal surface buff-yellow, curry-yellow, cinnamon, orange-brown to reddish brown, with one or more vinaceous brown, dark blue

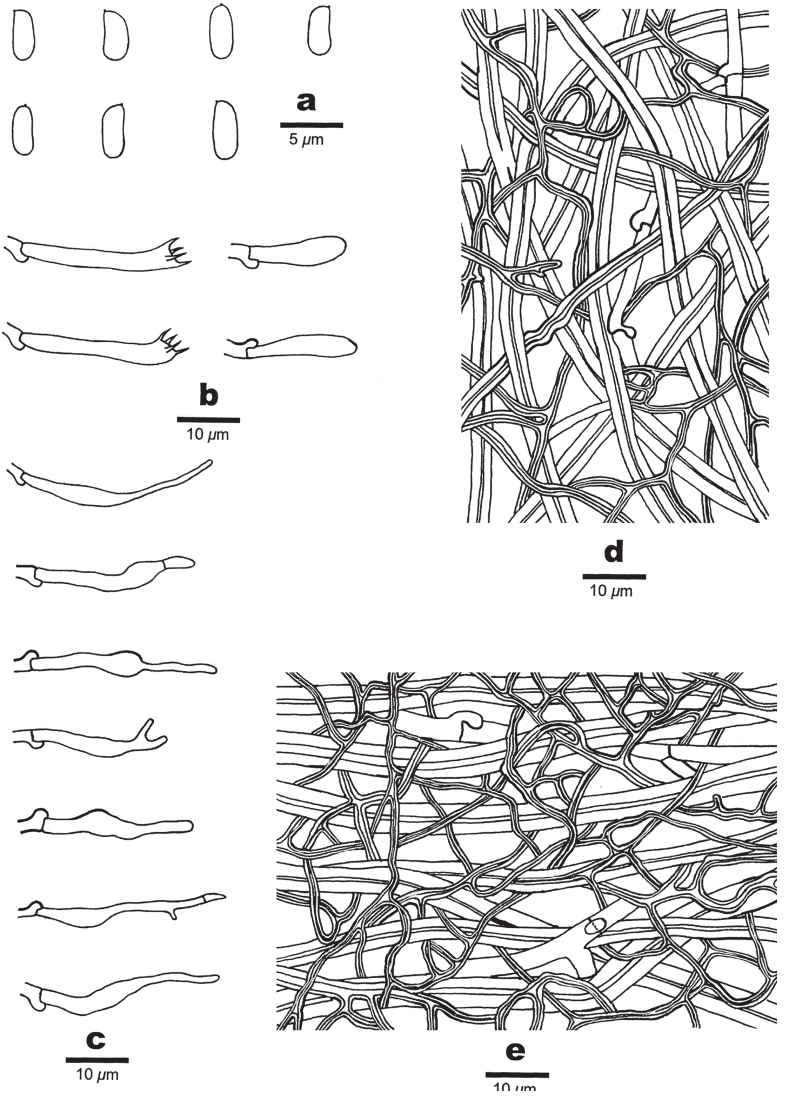

Fig. 3. *Neofomitella polyzonata* (drawn from the holotype).
a: Basidiospores. b: Basidia and basidioles. c: Cystidioles.
d: Hyphae from trama. e: Hyphae from context.

to almost black zones, finely velutinate, concentrically zonate; white to cream outgrowth occasionally spreading from the base with age. Margin cream, buff to buff-yellow, usually acute or slightly wavy. Pore surface cream to buff when

fresh, buff to yellowish brown when dry or bruised; sterile margin indistinct, white to cream, up to 0.5 mm wide; pores round, 3–4 per mm; dissepiments thin, entire. Context buff to yellowish brown, hard corky, azonate, up to 3 mm thick, a more or less dark agglutinated crust present as black zones in context towards upper surface. Tube layer concolorous with pore surface, up to 3 mm long.

Hyphal structure — Hyphal system trimitic; generative hyphae bearing clamp connections; skeletal and binding hyphae IKI–, CB–; tissue turning into black in KOH.

Context — Generative hyphae in context infrequent, colorless, thin-walled, moderately branched, 1.5–3 μm in diam; skeletal hyphae in context dominant, colorless to pale yellowish brown, thick-walled with a narrow lumen to subsolid, occasionally branched, straight, more or less regularly arranged, 3–5 μm in diam; binding hyphae in context abundant, colorless to pale yellowish brown, thick-walled with a narrow lumen to subsolid, flexuous, frequently branched, interwoven, 1–2.5 μm in diam.

Tubes — Generative hyphae infrequent, colorless, thin-walled, moderately branched, 1.2–2 μm in diam; skeletal hyphae in trama dominant, colorless to pale yellowish brown, thick-walled, occasionally branched, more or less straight, interwoven, 2.4–4 μm in diam; binding hyphae in trama colorless to pale yellowish brown, thick-walled with a narrow lumen to subsolid, flexuous, frequently branched, interwoven, 1–2 μm in diam. Cystidia absent, while cystidioles present, fusoid to tubular, sometimes tips of cystidioles branched and septate, colorless, thin-walled, 22–34 × 2.5–4.5 μm; basidia clavate, bearing four sterigmata and a basal clamp connection, 18–24 × 3.5–5 μm; basidioles in shape similar to basidia, but distinctly smaller.

Spores — Basidiospores cylindrical, colorless, thin-walled, smooth, IKI–, CB–, (3.8–)3.9–5 × (1.8–)1.9–2.1(–2.5) μm, L = 4.34 μm, W = 2.04 μm, Q = 2.13 (n = 9/1).

Type of rot —White rot.

Additional specimens examined — **CHINA**. **Fujian Province**, Wuyi Mountains, Longfenggu Forest Park, on fallen angiosperm trunk, 27 Aug 2006, B.K. Cui 4124 (BJFC 485, IFP 1196); Wuyishan Nature Reserve, Taoyuanyu, on fallen angiosperm trunk, 24 Aug 2006, Y.C. Dai 7376 (IFP 11887); **Hunan Province**, Shimen County, Hupingshan Nature Reserve, on fallen angiosperm trunk, 16 Sep 2009, Y.C. Dai 11360 (BJFC 7283); **Jiangxi Province**, Fenyi County, Dagang Mountain, on fallen trunk of *Cyclobalanopsis blakei*, 18 Sep 2008, Y.C. Dai 10420 (BJFC 4669).

Neofomitella rhodophaea (Lév.) Y.C. Dai, Hai J. Li & Vlasák, **comb. nov.** Figs 2d,e

MycoBank MB 804800

≡ *Polyporus rhodophaeus* Lév., Ann. Sci. Nat., Bot., 3e Sér., 2: 190 (1844).

≡ *Fomitella rhodophaea* (Lév.) T. Hatt., Mycoscience 46: 305 (2005).

Specimens examined — **JAPAN**. **Kagoshima Pref.**, Kimotsuki-Gun, Uchindura, Oct 1962, K. Aoshima (BJFC: ex. O 10866); **Tokyo**, Meguro, 15 Oct 1943 (BJFC: ex. TFM F-10861); **MALAYSIA**. **Negeri Sembilan**, Pasoh, Sembilan For. Nat. Res., 25 Dec 1997, T. Hattori (BJFC: ex. TFM 18313).

Other Specimens examined — ***Fomitella supina*** (Fig. 2f): **BRAZIL**. **Alagoas State**, Pilar Municipality, Reserva Particular do patrimonio Natural (PPPN) São Pedro, on dead hardwood, Oct 2000, B. Tatiana, N. Gibertoni 357 (BJFC: ex. O 10849). **COLOMBIA**. **Dept. de Antioquia**, Municipio Caldas finca, alt. 1700 m, 25 Jun 1978, L. Ryvarden 16 590 (BJFC: ex. O 10769). **GUATEMALA**. Lago Atitlán, on hard wood, J. Vlasák JV0610. **PANAMA**. Ensenada de Santa Cruz. Parque Nac. de Coiba, 17 Nov 1996, M. Nunez 1183 (BJFC: ex. O 10770). **PUERTO RICO**. Toro Negro, Commonwealth For., on deciduous wood, 24 Jun 1996, L. Ryvarden 39 027 (BJFC: ex. O 10772).

Discussion

The new genus *Neofomitella* is composed of two distinct lineages, one comprising *Neofomitella rhodophaea* and *N. fumosipora* and the other *N. polyzonata*, newly described from China. The main morphological characters of *Fomitella supina* and the three *Neofomitella* species are presented in Table 2. Like *Neofomitella polyzonata*, *N. fumosipora* has more or less brown basidiocarps; however, it has a glabrous pileal surface and smaller pores (7–9 per mm; Hattori 2005). All three *Neofomitella* species show distinctly crusted basidiocarps with a cuticle that develops from base to margin (Fig. 2a-e). In *F. supina* the cuticle also develops from the base but does not usually extend to the very margin (Fig. 2f).

Neofomitella is phylogenetically close to several *Microporus* species (Fig. 1). Although *Microporus* also has a trimitic hyphal system, colorless, thin-walled, smooth, non-dextrinoid, inamyloid basidiospores, its species usually produce stipitate basidiocarps with a white to cream context (Gilbertson & Ryvarden 1986; Núñez & Ryvarden 2001). Its type species, *M. perula* P. Beauv. [= *M. xanthopus* (Fr.) Kuntze], also has an encrusted pileal surface, but its centrally or laterally stipitate and usually infundibuliform basidiocarps, distinctly small pores, and white context (Núñez & Ryvarden 2001) clearly differentiate it from *Neofomitella* species.

Morphologically, *Coriolopsis* shares many features with *Fomitella* and *Neofomitella*, such as a more or less brown context, trimitic hyphal system with clamped generative hyphae, colorless basidiospores, and causing a white rot (Gilbertson & Ryvarden 1986; Núñez & Ryvarden 2001; Hattori 2005). However, phylogenetic analysis shows *Coriolopsis* as polyphyletic with its type species, *Polyporus occidentalis* Klotzsch [≡ *Coriolopsis occidentalis* (Klotzsch) Murrill; = *Trametes polyzona* (Pers.) Justo], clustering within the *Trametes* clade and distinctly separated from *Fomitella* and *Neofomitella* (Fig. 1).

Table 2. Main morphological characters of *Fomitella* and *Neofomitella* species.

Species	Basidiocarps[1]	Pores (/mm)	Basidiospores[2] (µm)	Cystidioles[3]	Distribution[4]
F. supina	A/P, V then G	5–7	6.5–9 × 2.4–3.5, C	–	T/S, America, Africa
N. fumosipora	A/P, G	6–10	3–4 × 1.7–2.2, C/OE	+	T/S, Asia
N. polyzonata	A, V	3–4	3.9–5 × 1.9–2.1, C	+	S/WT, China
N. rhodophaea	A/P, G	7–8	3.5–4.5 × 2.5–3, OE	–	T, also S/WT, Asia, Africa

[1] A = annual, P = perennial, G = glabrous, V = velutinate; [2] C = cylindrical, OE = oblong-ellipsoid; [3] + = presence, – = absence; [4] T = tropics, S = subtropics, WT = warm-temperate.

The transfer of this taxon to *Trametes* was suggested by Corner (1989) and validated by Justo & Hibbett (2011). *Coriolopsis strumosa* (Fr.) Ryvarden usually has encrusted basidiocarps that are similar to *Neofomitella*, but *C. strumosa* has a soft corky, olivaceous-brown, umber or hazel-brown context and distinctly larger basidiospores (7–10 × 3–4 µm; Núñez & Ryvarden 2001; Li 2013).

Funalia species cluster in the same clade with *Fomitella*. Both genera share trimitic hyphal system and more or less similar basidiospores, but *Funalia* species usually produce a strongly tomentose to hispid pileal surface, a white, cream to straw colored context, and cyanophilous skeletal hyphae (Niemelä et al. 1992; Dai 1996).

Hexagonia has pileate brown basidiocarps, tissues that darken in KOH, a trimitic hyphal system, and colorless thin-walled basidiospores similar to those in *Fomitella* and *Neofomitella* (Núñez & Ryvarden 2001). However, *Hexagonia* species usually have larger hexagonal pores and distinctly larger basidiospores (usually longer than 10 µm; Gilbertson & Ryvarden 1986; Núñez & Ryvarden 2001).

No sequences of *Fomitella malaysiana* are available at present. The distinctly encrusted pileal surface (Hattori & Sotome 2013) indicates that this species may belong to *Neofomitella*. Further molecular studies are needed to resolve its taxonomic and phylogenetic position.

Key to species of *Neofomitella*

1. Pores 3–4 per mm ..... *N. polyzonata*
1. Pores 6–10 per mm 2
2. Basidiospores 1.7–2.2 µm wide ..... *N. fumosipora*
2. Basidiospores 2.5–3 µm wide ..... *N. rhodophaea*

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Literature cited

Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, Langer G. 2005. The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (*Homobasidiomycetes*). Systematics and Biodiversity 3: 113–157. http://dx.doi.org/10.1017/S1477200005001623

Cao Y, Wu SH, Dai YC. 2012. Species clarification of the prize medicinal *Ganoderma* mushroom "Lingzhi". Fungal Diversity 56: 49–62. http://dx.doi.org/10.1007/s13225-012-0178-5

Chenna R, Sugawara H, Koike T, Lopez R, Gibson TJ, Higgins DG, Thompson JD. 2003. Multiple sequence alignment with the Clustal series of programs. Nucleic Acids Research 31: 3497–3500. http://dx.doi.org/10.1093/nar/gkg500

Corner, EJH. 1989. Ad Polyporaceas 6. The genus *Trametes*. Beihefte zur Nova Hedwigia 97: 1–197 .

Cui BK, Dai YC. 2008a. *Skeletocutis luteolus* sp. nov. from southern and eastern China. Mycotaxon 104: 97–101.

Cui BK, Dai YC. 2008b. Wood-rotting fungi in eastern China 2. A new species of *Fomitiporia* (*Basidiomycota*) from Wanmulin Nature Reserve, Fujian Province. Mycotaxon 105: 343–348.

Cui BK, Zhao CL. 2012. Morphological and molecular evidence for a new species of *Perenniporia* (*Basidiomycota*) from Tibet, southwestern China. Mycoscience 53: 365–372. http://dx.doi.org/10.1007/s10267-011-0180-x

Cui BK, Dai YC, Decock C. 2007. A new species of *Perenniporia* (*Basidiomycota*, *Aphyllophorales*) from eastern China. Mycotaxon 99: 175–180.

Cui BK, Yuan HS, Dai YC. 2008. Wood-rotting fungi in eastern China 1. Polypores from Wuyi Mountains, Fujian Province. Sydowia 60: 25–40.

Dai YC. 1996. Changbai wood-rotting fungi 7. A check list of the polypores. Fungal Science 11: 79–105.

Dai YC, Cui BK. 2005. Two new species of the *Hymenochaetaceae* from eastern China. Mycotaxon 94: 341–347.

Felsenstein J. 1985. Confidence intervals on phylogenies: an approach using the bootstrap. Evolution 39: 783–791.

Gilbertson RL, Ryvarden L. 1986. North American polypores 1. *Abortiporus–Lindtneria*. Fungiflora, Oslo. 433 p.

Hattori T. 2005. Type studies of the polypores described by E.J.H. Corner from Asia and West Pacific Areas 7. Species described in *Trametes* (1). Mycoscience 46: 303–312. http://dx.doi.org/10.1007/s10267-005-0250-z

Hattori T, Sotome K. 2013. Type studies of the polypores described by E.J.H. Corner from Asia and West Pacific areas VIII. Species described in *Trametes* (2). Mycoscience 54: 297–308. http://dx.doi.org/ 10.1016/j.myc.2012.10.008

He SH, Dai YC. 2012. Taxonomy and phylogeny of *Hymenochaete* and allied genera of *Hymenochaetaceae* (*Basidiomycota*) in China. Fungal Diversity 56:77–93. http://dx.doi.org/10.1007/s13225-012-0174-9

Huelsenbeck JP, Crandall KA. 1997. Phylogeny estimation and hypothesis testing using maximum likelihood. Annual Review of Ecology, Evolution, and Systematics 28: 437–466. http://dx.doi.org/10.1146/annurev.ecolsys.28.1.437

Justo A, Hibbett DS. 2011. Phylogenetic classification of *Trametes* (*Basidiomycota*, *Polyporales*) based on a five-marker dataset. Taxon 60: 1567–1583.

Larsson KH. 2007. Re-thinking the classification of corticioid fungi. Mycological Research 111: 1040–1063. http://dx.doi.org/10.1016/j.mycres.2007.08.001

Larsson KH, Larsson E, Kõljalg U. 2004. High phylogenetic diversity among corticioid homobasidiomycetes. Mycological Research 108: 983–1002. http://dx.doi.org/10.1017/S0953756204000851

Li HJ. 2013. Taxonomy and phylogeny of *Trametes* and related genera in China. PhD thesis, Beijing Forestry University. Beijing.

Liu YL, Whelen S, Hall BD. 1999. Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Molecular Biology and Evolution 16: 1799–1808. http://dx.doi.org/ 10.1093/oxfordjournals.molbev.a026092

Matheny PB. 2005. Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*; *Agaricales*). Molecular Phylogenetics and Evolution 35: 1–20. http://dx.doi.org/ 10.1016/j.ympev.2004.11.014

Miettinen O, Rajchenberg M. 2012. *Obba* and *Sebipora*, new polypore genera related to *Cinereomyces* and *Gelatoporia* (*Polyporales*, *Basidiomycota*). Mycological Research 11: 131–147. http://dx.doi.org/ 10.1007/s11557-010-0736-8

Murrill WA. 1905. The *Polyporaceae* of North America 11. A synopsis of the brown pileate species. Bulletin of the Torrey Botanical Club 32: 353–371.

Murrill WA. 1908. *Polyporaceae*. North American Flora 9(2): 73–132.

Niemelä T, Kotiranta H, Penttilä R. 1992. New records of rare and threatened polypores in Finland. Karstenia 32: 81–94.

Núñez M, Ryvarden L. 2001. East Asian polypores 2. *Polyporaceae* s. lato. Synopsis Fungorum 14: 170–522.

Nylander JAA. 2004. MrModeltest 2.2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Petersen JH. 1996. Farvekort. The Danish Mycological Society's colour-chart. Foreningen til Svampekundskabens Fremme, Greve. 6 p.

Posada D, Crandall KA. 1998. MODELTEST: testing the model of DNA substitution. Bioinformatics 14: 817–818.

Posada D, Crandall KA. 2001. Selecting the best-fit model of nucleotide substitution. Systematic Biology 50: 580–601. http://dx.doi.org/ 10.1080/106351501750435121

Ronquist F, Huelsenbeck JP. 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574. http://dx.doi.org/ 10.1093/bioinformatics/btg180

Ryvarden L, Gilbertson RL. 1993. European polypores. Synopsis Fungorum 6: 1–741.

Swofford DL. 2002. PAUP: Phylogenetic analysis using parsimony, version 4.0b10. Sinauer Associates, Inc. Publishers, Sunderland.

Wang B, Dai YC, Cui BK, Du P, Li HJ. 2009. Wood-rotting fungi in eastern China 4. Polypores from Dagang Mountains, Jiangxi Province. Cryptogamie, Mycologie 30: 233–241.

Wang B, Cui BK, Li HJ, Du P, Jia BS. 2011. Wood-rotting fungi in eastern China 5. Polypore diversity in Jiangxi Province. Annales Botanici Fennici 48: 237–246. http://dx.doi.org/10.5735/085.048.0304

White TJ, Bruns TD, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: MA Innis et al. (eds). PCR protocols, a guide to methods and applications. Academic, San Diego.